



1

SEQUENCE LISTING

101725, 284

<110> ADLER, JON ELLIOT
LI, XIAODONG
STASZEWSKI, LENA
O'CONNELL, SHAWN
ZOZULYA, SERGEY

<120> T1R TASTE RECEPTORS AND GENES ENCODING SAME

<130> 078003-0280681

<140> 10/035,045

<141> 2002-01-03

<150> 60/259,227

<151> 2001-01-03

<150> 60/284,547

<151> 2001-04-19

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 876

<212> DNA

<213> Homo sapiens

<400> 1

agcctggcag	tggcctcagg	cagagtctga	cgcgcacaaa	ctttcaggcc	caggaagcga	60
ggacaccact	ggggccccag	ggtgtggcaa	gtgaggatgg	caagggtttt	gctaaacaaa	120
tcctctgccc	gctccccgcc	ccgggctcac	tccatgtgag	gccccagtcg	gggcagccac	180
ctgccgtgcc	tgttgggaagt	tgccctctgcc	atgctggggcc	ctgctgtcct	gggcctcagc	240
ctctggggctc	tcctgcaccc	tgggacgggg	gccccattgt	gcctgtcaca	gcaacttagg	300
atgaaggggg	actacgtgct	gggggggctg	ttccccctgg	gcgaggccga	ggaggctggc	360
ctccgcagcc	ggacacggcc	cagcagccct	gtgtgcacca	ggtacagagg	tgggacggcc	420
tgggtcgggg	tcagggtgac	caggtctggg	gtgctcctga	gctggggccg	aggtggccat	480
ctgcggttct	gtgtggcccc	aggttctcct	caaacggcct	gctctgggca	ctggccatga	540
aaatggccgt	ggaggagatc	aacaacaagt	cggatctgct	gccccgggctg	cgcctgggct	600
acgacctctt	tgatacgtgc	tcggagcctg	tggtagccat	gaagcccagc	ctcatgttcc	660
tggccaaggc	aggcagccgc	gacatcgccg	cctactgcaa	ctacacgcag	taccagcccc	720
gtgtgctggc	tgtcatcggg	ccccactcgt	cagagctcgc	catgggtcacc	ggcaagttct	780
tcagcttctt	cctcatgccc	cagtggggcg	ccccccacca	tcaccacccc	ccaaccaacc	840
cctgccccgt	gggagccccct	tgtgtcagga	gaatgc			876

<210> 2

<211> 2687

<212> DNA

<213> Homo sapiens

<400> 2

tacatgcacc	ccaccagcc	ctgccctggg	agccctgtgt	cagaagatgc	tcttggcctt	60
gcaggtcagc	tacgggtgcta	gcatggagct	gctgagcgcc	cgggagacct	tccccctctt	120
cttccgcacc	gtgcccagcg	accgtgtgca	gctgacggcc	gccgcggagc	tgtgtcagga	180
gttcgggtgg	aactgggtgg	ccgccctggg	cagcgacgac	gagtacggcc	ggcagggcct	240

gagcatcttc	tggccctgg	ccgcggcacg	cggcatctgc	atcgcgacg	agggcctggt	300
gccgtgccc	cgtgccgatg	actcgcggt	ggggaagggtg	caggacgtcc	tgcaccaggt	360
gaaccagagc	agcgtgcagg	tgggtgctgct	gttcgcctcc	gtgcacgccg	cccacgcctt	420
cttcaactac	agcatcagca	gcaggctctc	gcccgaagggtg	tgggtggcca	gcgaggcctg	480
gctgacctct	gacctgggtca	tggggctgcc	cggcatggcc	cagatgggca	cggtgcttgg	540
cttctccag	aggggtgccc	agctgcacga	gttccccag	tacgtgaaga	cgacactggc	600
cctggccacc	gacccggcct	tctgctctgc	cctgggagag	agggagcagg	gtctggaggga	660
ggacgtgggtg	ggccagcgct	gcccgcagtg	tgactgcatc	acgtgacaga	acgtgagcgc	720
agggctaaat	caccaccaga	cgttctctgt	ctacgcagct	gtgtatagcg	tggcccaggc	780
cctgcacaac	actcttcagt	gcaacgcctc	aggctgcccc	gcgcaggacc	ccgtgaagcc	840
ctggcagggtg	agcccgggag	atgggggtgt	gctgtcctct	gcatgtgccc	agggcaccag	900
gcacggccac	cacgcctgag	ctggagggtg	ctggcggtc	agccccgtcc	ccgccccgca	960
gctcctggag	aacatgtaca	acctgacctt	ccacgtgggc	gggctgccgc	tgcggttcga	1020
cagcagcgga	aacgtggaca	tggagtacga	cctgaagctg	tgggtgtggc	agggctcagt	1080
gcccaggctc	cacgacgtgg	gcaggttcaa	cggcagcctc	aggacagagc	gcctgaagat	1140
ccgctggcac	acgtctgaca	accagggtgag	gtgagggtgg	gtgtgccagg	cgtgcccgtg	1200
gtagccccc	cggcaggggc	cagcctgggg	gtggggggcc	ttccagtctc	ccgtgggcat	1260
gcccagccga	gcagagccag	accccaggcc	tgtgcgcaga	agccccgtgc	ccggtgctcg	1320
cggcagtgcc	aggagggcca	ggtgcgcggg	gtcaaggggt	tccactcctg	ctgctacgac	1380
tgtgtggact	gcgaggcggg	cagctaccgg	caaaaccag	gtgagccgcc	ttcccggcag	1440
gcgggggtgg	gaacgcagca	ggggagggtc	ctgccaagtc	ctgactctga	gaccagagcc	1500
cacagggtac	aagacgaaca	cccagcgccc	ttctcctctc	tcacagacga	catcgccctg	1560
accttttgtg	gccaggatga	gtggtcccc	gagcgaagca	cacgtgctt	ccgccgcagg	1620
tctcggttcc	tggcatgggg	cgagccggct	gtgctgctgc	tgctcctgct	gctgagcctg	1680
gcgctgggccc	ttgtgctggc	tgttttgggg	ctgttcgttc	accatcgggg	cagccactg	1740
gttcaggcct	cggggggggc	cctggcctgc	tttggcctgg	tgtgcctggg	cctggtctgc	1800
ctcagcgctc	tcctgttccc	tggccagccc	agccctgccc	gatgcctggc	ccagcagccc	1860
ttgtcccacc	tcccgtcac	gggctgcctg	agcacactct	tcctgcaggc	ggccgagatc	1920
ttcgtggagt	cagaactgcc	tctgagctgg	gcagaccggc	tgagtggctg	cctgcggggg	1980
ccctgggcct	ggetgggtgg	gctgctggcc	atgctgggtg	aggtcgcact	gtgcacctgg	2040
tacctggtgg	ccttcccggc	ggagggtggg	acggactggc	acatgctgcc	cacggaggcg	2100
ctggtgcact	gccgcacacg	ctcctgggtc	agcttcggcc	tagcgcacgc	caccaatgcc	2160
acgttggect	ttctctgctt	cctgggcact	ttcctgggtg	ggagccagcc	gggctgctac	2220
aaccgtgccc	gtggcctcac	ctttgccatg	ctggccctact	tcacacactg	gggtctccttt	2280
gtgcccctcc	tggccaatgc	gcagggtggc	ctcagggccc	ccgtgcagat	ggggcgcctc	2340
tgctctgtg	tcctgggcct	cctggctgcc	ttccacctgc	ccagggtgta	ctgctcctg	2400
cggcagccag	ggctcaaacac	ccccaggttc	ttcctgggag	ggggccctgg	ggatgccccaa	2460
ggccagaatg	acgggaacac	aggaaatcag	gggaaacatg	agtgaaccaa	ccctgtgatc	2520
tcagccccgg	tgaaccagga	cttagctgcg	atcccccca	agccagcaat	gacccgtgtc	2580
tcgctacaga	gaccctccc	ctctaggttc	tgacccagg	ttgtctcctg	accctgaccc	2640
cacagtgagc	cctaggcctg	gagcacgtgg	acacccctgt	gaccatc		2687

<210> 3

<211> 2559

<212> DNA

<213> Homo sapiens

<400> 3

atgctggggc	ctgctgtcct	gggcctcagc	ctctgggctc	tcctgcaccc	tgggacgggg	60
gccccattgt	gcctgtcaca	gcaacttagg	atgaaggggg	actacgtgct	gggggggctg	120
ttccccctgg	gcgaggccga	ggaggctggc	ctccgcagcc	ggacacggcc	cagcagccct	180
gtgtgcacca	ggttctcctc	aaacggcctg	ctctgggcac	tggccatgaa	aatggcctgt	240
gaggatca	acaacaagtc	ggatctgctg	cccgggctgc	gcctgggcta	cgacctcttt	300
gatacgtgct	ggagccctgt	ggtggccatg	aagcccagcc	tcattgtcct	ggccaaggca	360
ggcagccggc	acatcgccgc	ctactgcaac	tacacgcagt	accagccccg	tgtgtgggt	420
gtcatcgggc	cccactcgtc	agagctcgcc	atggtcaccg	gcaagttctt	cagcttcttc	480
ctcatgcccc	aggtcagcta	cggtgctagc	atggagctgc	tgagcgcccc	ggagaccttc	540

```

ccctccttct tccgcaccgt gccagcgac cgtgtgcagc tgacggccgc cgcggagctg 600
ctgcaggagt tgggctggaa ctgggtggcc gccctgggca gcgacgacga gtacggcccg 660
cagggcctga gcattcttct ggccctggcc gcggcacgcg gcattctgcat cgcgcacgag 720
ggcctgggtgc cgctgcccgc tgccgatgac tcgcggtgg ggaaggtgca ggacgtcctg 780
caccaggtga accagagcag cgtgcaggtg gtgctgctgt tcgcctccgt gcacggccgc 840
cacgccctct tcaactacag catcagcagc aggtctctgc ccaaggtgtg ggtggccagc 900
gaggcctggc tgacctctga cctggtcatg gggctgcccg gcatggccca gatgggcacg 960
gtgcttggtc tcctccagag gggtgcccag ctgcacgagt tccccagta cgtgaagacg 1020
cacctggccc tggccaccga cccggccttc tgctctgccc tgggcgagag ggagcagggg 1080
ctggaggagg acgtgggtgg ccagcgctgc ccgcagtgtg actgcatcac gctgcagaac 1140
gtgagcgagc ggctaaatca ccaccagacg ttctctgtct acgcagctgt gtatagctgt 1200
gccagggccc tgcacaacac tcttcagtgc aacgcctcag gctgccccgc gcaggacccc 1260
gtgaagccct ggcagctcct ggagaacatg tacaacctga ccttccacgt gggcgggctg 1320
ccgctgcggt tcgacagcag cggaaacgtg gacatggagt acgacctgaa gctgtgggtg 1380
tggcaggggt cagtgccacg gctccacgac gtgggcaggt tcaacggcag cctcaggaca 1440
gagcgccctga agatccgctg gcacacgtct gacaaccaga agcccgtgtc ccggtgctcg 1500
cggcagtgcc aggagggcca ggtgcgcccg gtcaaggggg tccactcctg ctgtacgac 1560
tgtgtggact gcgaggcggg cagctaccgg caaaacccag acgacatcgc ctgcaccttt 1620
tgtggccagg atgagtggtc cccggagcga agcacacgct gcttccgccc caggtctcgg 1680
ttcctggcat ggggcgagcc ggctgtgctg ctgctgtctc tgctgtgag cctggcgctg 1740
ggccttgtgc tggtgctttt ggggctgttc gttcaccatc gggacagccc actggttcag 1800
gcctcggggg ggcccctggc ctgctttggc ctggtgtgcc tgggcctggt ctgcctcagc 1860
gtcctcctgt tccctggcca gccagccct gccgatgcc tggcccagca gcccttgtcc 1920
cacctcccgc tcacgggctg cctgagcaca ctcttctgc aggcggccga gatctctgtg 1980
gagtcagaac tgctctgag ctgggcagac cggctgagtg gctgcctgcg ggggccctgg 2040
gcctggctgg ttgtgtgct ggccatgctg gtggaggtcg cactgtgcac ctggtacctg 2100
gtggccttcc cgcggaggt ggtgacggac tggcacatgc tgcccacgga ggcgctggtg 2160
cactgcgcga cacgtcctg ggtcagcttc ggcctagcgc acgccaccaa tgccacgtg 2220
gcctttctct gcttcttggg cactttctct gtgcggagcc agccgggctg ctacaacctg 2280
gcccgctggc tcacctttgc catgctggcc tacttcatca cctgggtctc cttgtgccc 2340
ctcctggcca atgtgcaggt ggtcctcagg cccgcctgac agatgggcgc cctcctgctc 2400
tgtgtcctgg gcactcctgg tccttccac ctgcccaggt gttacctgct catgcggcag 2460
ccagggtca acaccccga gttcttctg ggagggggcc ctggggatgc ccaaggccag 2520
aatgacggga acacaggaaa tcaggggaaa catgagtga 2559

```

<210> 4
 <211> 852
 <212> PRT
 <213> Homo sapiens

```

<400> 4
Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His
 1             5             10             15

Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys
          20             25             30

Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
          35             40             45

Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
          50             55             60

Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
          65             70             75             80

```

Glu	Glu	Ile	Asn	Asn	Lys	Ser	Asp	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly	
				85					90					95		
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Ala	Met	Lys	Pro	
			100					105					110			
Ser	Leu	Met	Phe	Leu	Ala	Lys	Ala	Gly	Ser	Arg	Asp	Ile	Ala	Ala	Tyr	
		115					120					125				
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	
		130					135					140				
His	Ser	Ser	Glu	Leu	Ala	Met	Val	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	
145					150					155					160	
Leu	Met	Pro	Gln	Val	Ser	Tyr	Gly	Ala	Ser	Met	Glu	Leu	Leu	Ser	Ala	
				165					170					175		
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val	
			180					185					190			
Gln	Leu	Thr	Ala	Ala	Ala	Glu	Leu	Leu	Gln	Glu	Phe	Gly	Trp	Asn	Trp	
		195					200					205				
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Glu	Tyr	Gly	Arg	Gln	Gly	Leu	Ser	
		210					215					220				
Ile	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	
225					230					235					240	
Gly	Leu	Val	Pro	Leu	Pro	Arg	Ala	Asp	Asp	Ser	Arg	Leu	Gly	Lys	Val	
			245					250					255			
Gln	Asp	Val	Leu	His	Gln	Val	Asn	Gln	Ser	Ser	Val	Gln	Val	Val	Leu	
			260					265					270			
Leu	Phe	Ala	Ser	Val	His	Ala	Ala	His	Ala	Leu	Phe	Asn	Tyr	Ser	Ile	
		275					280					285				
Ser	Ser	Arg	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Leu	
		290					295					300				
Thr	Ser	Asp	Leu	Val	Met	Gly	Leu	Pro	Gly	Met	Ala	Gln	Met	Gly	Thr	
305					310					315					320	
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Gln	Leu	His	Glu	Phe	Pro	Gln	
			325					330					335			
Tyr	Val	Lys	Thr	His	Leu	Ala	Leu	Ala	Thr	Asp	Pro	Ala	Phe	Cys	Ser	
			340					345					350			
Ala	Leu	Gly	Glu	Arg	Glu	Gln	Gly	Leu	Glu	Glu	Asp	Val	Val	Gly	Gln	
		355					360					365				
Arg	Cys	Pro	Gln	Cys	Asp	Cys	Ile	Thr	Leu	Gln	Asn	Val	Ser	Ala	Gly	
		370					375					380				

Leu Asn His His Gln Thr Phe Ser Val Tyr Ala Ala Val Tyr Ser Val
 385 390 395 400
 Ala Gln Ala Leu His Asn Thr Leu Gln Cys Asn Ala Ser Gly Cys Pro
 405 410 415
 Ala Gln Asp Pro Val Lys Pro Trp Gln Leu Leu Glu Asn Met Tyr Asn
 420 425 430
 Leu Thr Phe His Val Gly Gly Leu Pro Leu Arg Phe Asp Ser Ser Gly
 435 440 445
 Asn Val Asp Met Glu Tyr Asp Leu Lys Leu Trp Val Trp Gln Gly Ser
 450 455 460
 Val Pro Arg Leu His Asp Val Gly Arg Phe Asn Gly Ser Leu Arg Thr
 465 470 475 480
 Glu Arg Leu Lys Ile Arg Trp His Thr Ser Asp Asn Gln Lys Pro Val
 485 490 495
 Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys
 500 505 510
 Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp Cys Glu Ala Gly Ser
 515 520 525
 Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys Thr Phe Cys Gly Gln Asp
 530 535 540
 Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys Phe Arg Arg Arg Ser Arg
 545 550 555 560
 Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Leu Leu Leu Leu Leu Leu
 565 570 575
 Ser Leu Ala Leu Gly Leu Val Leu Ala Ala Leu Gly Leu Phe Val His
 580 585 590
 His Arg Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro Leu Ala Cys
 595 600 605
 Phe Gly Leu Val Cys Leu Gly Leu Val Cys Leu Ser Val Leu Leu Phe
 610 615 620
 Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu Ala Gln Gln Pro Leu Ser
 625 630 635 640
 His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala
 645 650 655
 Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu
 660 665 670
 Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala
 675 680 685

Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro
 690 695 700
 Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
 705 710 715 720
 His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr
 725 730 735
 Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg
 740 745 750
 Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met
 755 760 765
 Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn
 770 775 780
 Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu
 785 790 795 800
 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
 805 810 815
 Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly
 820 825 830
 Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln
 835 840 845
 Gly Lys His Glu
 850

<210> 5
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (3)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (9)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (12)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (18)
 <223> a, t, c, g, other or unknown

<400> 5
 cgnttyytng cntggggnga rcc

23

<210> 6
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (3)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (6)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (18)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (21)
 <223> a, t, c, g, other or unknown

<400> 6
 cgngcncgrt trtarcanc ngg

23

<210> 7
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 7
 Arg Phe Leu Ala Trp Gly Glu Pro Ala
 1 5

<210> 8
 <211> 8
 <212> PRT
 <213> Homo sapiens

<400> 8

Pro Gly Cys Tyr Asn Arg Ala Arg

1

5

<210> 9

<211> 552

<212> DNA

<213> Mus sp.

<400> 9

```

gtgctgtcac tctctctgct gctttgctg gtgctgggtc tagcactggc tgctctgggg 60
ctctctgtcc accactggga cagccctctt gtccaggcct caggcggctc acagttctgc 120
tttggcctga tctgcctagg cctcttctgc ctcagtgtcc ttctgttccc aggacggcca 180
agctctgccca gctgccttgc acaacaacca atggctcacc tccctctcac aggctgcctg 240
agcacactct tctgcaagc agctgagacc tttgtggagt ctgagctgcc actgagctgg 300
gcaaactggc tatgcagcta ccttcgggac tctggcctgc tagtggtact gttggccact 360
tttgtggagg cagcactatg tgcttggat ttgaccgctt caccagaagt ggtgacagac 420
tggtcagtcg tgcccacaga ggtactggag cactgccacg tgcgttcctg ggtcaacctg 480
ggcttggtgc acatcaccaa tgcaatggta gcttttctct gctttctggg cactttcctg 540
gtacaagacc ag                                     552

```

<210> 10

<211> 184

<212> PRT

<213> Mus sp.

<400> 10

```

Val Leu Ser Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu
 1               5               10               15
Ala Ala Leu Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln
          20               25               30
Ala Ser Gly Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu
          35               40               45
Phe Cys Leu Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser
          50               55               60
Cys Leu Ala Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu
          65               70               75               80
Ser Thr Leu Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu
          85               90               95
Pro Leu Ser Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Asp Ser Gly
          100              105              110
Leu Leu Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala
          115              120              125
Trp Tyr Leu Thr Ala Ser Pro Glu Val Val Thr Asp Trp Ser Val Leu
          130              135              140
Pro Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Asn Leu
          145              150              155              160

```


Gly Leu Val His Ile Thr Asn Ala Met Val Ala Phe Leu Cys Phe Leu
 165 170 175

Gly Thr Phe Leu Val Gln Asp Gln
 180

<210> 11
 <211> 558
 <212> DNA
 <213> Rattus sp.

<400> 11
 gtgctgtcac ttctcctgct gctttgcctg gtgctgggccc tgacactggc tgccctgggg 60
 ctctttgtcc actactggga cagccctctt gttcaggcct cagggtgggtc actgttctgc 120
 tttggcctga tctgcctagg cctcttctgc ctgagtgccc ttctgttccc aggacgacca 180
 cgctctgcca gctgccttgc ccaacaacca atggctcacc tccctctcac aggtctgctg 240
 agcacactct tcctgcaagc agccgagatc tttgtggagt ctgagctgcc actgagttgg 300
 gcaaaactggc tctgcagcta ccttcggggc ccctgggctt ggctgggtgg actgctggcc 360
 actcttgctg aggtgcact atgtgcctgg tactttgatgg ctttccctcc agaggtgggtg 420
 acagattggc aggtgctgcc cacggaggta ctggaacact gccgcatgcg ttctgggtc 480
 agcctgggct tgggtcacat caccaatgca ggggtagctt tcctctgctt tctgggcact 540
 ttctgtgtac aaagccag 558

<210> 12
 <211> 186
 <212> PRT
 <213> Rattus sp.

<400> 12
 Val Leu Ser Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu
 1 5 10 15
 Ala Ala Leu Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln
 20 25 30
 Ala Ser Gly Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu
 35 40 45
 Phe Cys Leu Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser
 50 55 60
 Cys Leu Ala Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu
 65 70 75 80
 Ser Thr Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu
 85 90 95
 Pro Leu Ser Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp
 100 105 110
 Ala Trp Leu Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys
 115 120 125
 Ala Trp Tyr Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln
 130 135 140

Val Leu Pro Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val
 145 150 155 160

Ser Leu Gly Leu Val His Ile Thr Asn Ala Gly Val Ala Phe Leu Cys
 165 170 175

Phe Leu Gly Thr Phe Leu Val Gln Ser Gln
 180 185

<210> 13

<211> 2577.

<212> DNA

<213> Rattus sp.

<400> 13

```

atgccggggtt tggctatctt gggcctcagt ctggctgctt tcctggagct tgggatgggg 60
tcctctttgt gtctgtcaca gcaattcaag gcacaagggg actatatatt ggggtggacta 120
tttcccttgg gcacaactga ggaggccact ctcaaccaga gaacacagcc caacggcatc 180
ctatgtacca ggttctcgcc ccttggtttg ttcctggcca tggctatgaa gatggctgta 240
gaggagatca acaatggatc tgccttgctc cctgggctgc gactgggcta tgacctgttt 300
gacacatgct cagagccagt ggtcaccatg aagcccagcc tcatgttcat ggccaagggtg 360
ggaagtcaaa gcattgctgc ctactgcaac tacacacagt accaaccctg ggaacacattt 420
gtcattgggtc cccactcatc agagcttgcc ctcatcacag gcaagtctct cagcttcttc 480
ctcatgccac aggtcagcta tagtgccagc atggatcggc taagtgaccg ggaacacattt 540
ccatccttct tccgcacagt gcccagtgac cgggtgcagc tgcaggccgt tgtgacactg 600
ttgcagaatt tcagctggaa ctgggtgggt gccttaggta gtgatgatga ctatggccgg 660
gaaggctgta gcatcttttc tggctctggc aactcacgag gtatctgcat tgcacacgag 720
ggcctgggtgc cacaacatga cactagtggc caacaattgg gcaagggtgg ggatgtgcta 780
cgccaagtga accaaagcaa agtacagggt gtgggtgctgt ttgcatctgc ccgtgctgtc 840
tactcccttt ttagctacag catccttcat gacctctcac ccaaggtagt ggtggccagt 900
gagtccctggc tgacctctga cctgggtcat acacttccca atattgcccg tgtgggcact 960
gttcttgggt ttctgcagcg cgggtgccct ctgcctgaat tttcccatTA tgtggagact 1020
cgcttggccc tagctgctga cccaacattc tgtgcctccc tgaaagctga gttggatctg 1080
gaggagcgcg tgatggggcc acgctgttca caatgtgact acatcatgct acagaacctg 1140
tcatctgggc tgatgcagaa cctatcagct gggcagttgc accaccaaat atttgcaacc 1200
tatgcagctg tgtacagtgt ggctcaggcc cttcacaaca ccctgcagtg caatgtctca 1260
cattgccaca catcagagcc tgttcaacct tggcagctcc tggagaacat gtacaatatg 1320
agtttccgtg ctcgagactt gacactgcag tttgatgcca aagggagtgat agacatggaa 1380
tatgacctga agatgtgggt gtggcagagc cctacacctg tactacatac tgtaggcacc 1440
ttcaacggca cccttcagct gcagcactcg aaaatgtatt ggccaggcaa ccaggtgcca 1500
gtctcccagt gctcccggca gtgcaaagat ggccagggtg gcagagtaaa gggctttcat 1560
tcctgctgct atgactgtgt ggactgcaag gcaggagagt accggaagca tccagatgac 1620
ttcacctgta ctccatgtgg caaggatcag tgggtcccag aaaaaagcac aacctgctta 1680
cctgcgaggc ccaagtttct ggcttggggg gagccagctg tgctgtcact tctcctgctg 1740
ctttgcttgg tgetgggctt gacactggct gccctggggc tctttgtcca ctactgggac 1800
agccctcttg ttcaggcctc aggtgggtca ctgttctgct ttggcctgat ctgcctaggc 1860
ctcttctgcc tcagtgtcct tctgttccca ggacgaccac gctctgccag ctgccttggc 1920
caacaaccaa tggctcacct cctctcaca ggctgctga gcacactctt cctgcaagca 1980
gccgagatct ttgtggagtc tgagctgcca ctgagttggg caaactggct ctgcagctac 2040
cttcggggcc cctgggcttg gctggtggtg ctgctggcca ctcttgtgga ggctgacta 2100
tgtgcttggg acttgatggc ttccctcca gaggtgggtg cagattggga ggtgctgccc 2160
acggaggtac tggaaactg cgcgatgcgt tctgggtca gcctgggctt ggtgcacatc 2220
accaatgcag tgtagctttt cctctgcttt ctgggcaact tccgtgtaca gagcagcct 2280
ggctgctata accgtgcccg tggcctcacc ttcgccaatgc tagcttattt catcatctgg 2340
gtctcttttg tgccctcct ggctaattgt caggtggcct accagccagc tgtgcagatg 2400
gggtctatct tattctgtgc cctgggcatc ctggccacct tccacctgcc caaatgctat 2460

```

gtactttctgt ggctgccaga gctcaacacc caggagttct tcctgggaag gagccccaag 2520
 gaagcatcag atgggaatag tggtagtagt gaggcaactc ggggacacag tgaatga 2577

<210> 14
 <211> 858
 <212> PRT
 <213> Rattus sp.

<400> 14

Met	Pro	Gly	Leu	Ala	Ile	Leu	Gly	Leu	Ser	Leu	Ala	Ala	Phe	Leu	Glu	
1				5					10					15		
Leu	Gly	Met	Gly	Ser	Ser	Leu	Cys	Leu	Ser	Gln	Gln	Phe	Lys	Ala	Gln	
			20					25					30			
Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Thr	Thr	Glu	Glu	
		35					40					45				
Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Gly	Ile	Leu	Cys	Thr	Arg	
	50					55					60					
Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val	
	65				70					75					80	
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly	
			85						90					95		
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Pro	
		100						105					110			
Ser	Leu	Met	Phe	Met	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr	
		115					120					125				
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	
	130					135					140					
His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	
145				150						155					160	
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp	
			165					170					175			
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val	
		180						185					190			
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp	
	195						200					205				
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser	
	210					215					220					
Ile	Phe	Ser	Gly	Leu	Ala	Asn	Ser	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	
225				230						235				240		
Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val	
				245					250					255		

Val	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	260	265	270	
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile	275	280	285	
Leu	His	Asp	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	290	295	300	
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	305	310	315	320
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His	325	330	335	
Tyr	Val	Glu	Thr	Arg	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Thr	Phe	Cys	Ala	340	345	350	
Ser	Leu	Lys	Ala	Glu	Leu	Asp	Leu	Glu	Glu	Arg	Val	Met	Gly	Pro	Arg	355	360	365	
Cys	Ser	Gln	Cys	Asp	Tyr	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu	370	375	380	
Met	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr	385	390	395	400
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	405	410	415	
Cys	Asn	Val	Ser	His	Cys	His	Thr	Ser	Glu	Pro	Val	Gln	Pro	Trp	Gln	420	425	430	
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	Arg	Ala	Arg	Asp	Leu	Thr	435	440	445	
Leu	Gln	Phe	Asp	Ala	Lys	Gly	Ser	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	450	455	460	
Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	465	470	475	480
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	His	Ser	Lys	Met	Tyr	Trp	Pro	Gly	485	490	495	
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	500	505	510	
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	515	520	525	
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	530	535	540	
Pro	Cys	Gly	Lys	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Thr	Cys	Leu	545	550	555	560

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser
 565 570 575
 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu
 580 585 590
 Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
 595 600 605
 Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
 610 615 620
 Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala
 625 630 635 640
 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
 645 650 655
 Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
 660 665 670
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
 675 680 685
 Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
 690 695 700
 Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
 705 710 715 720
 Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
 725 730 735
 Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
 740 745 750
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
 755 760 765
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
 770 775 780
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
 785 790 795 800
 Gly Ala Ile Leu Phe Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu
 805 810 815
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Glu Leu Asn Thr Gln Glu
 820 825 830
 Phe Phe Leu Gly Arg Ser Pro Lys Glu Ala Ser Asp Gly Asn Ser Gly
 835 840 845
 Ser Ser Glu Ala Thr Arg Gly His Ser Glu
 850 855

<210> 15
 <211> 8194
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1251)..(1300)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1951)..(2000)
 <223> a, t, c, g, other or unknown

<400> 15
 gagaatctcg cgagatcccg tcgggtccgcc ccgctgccct cccagctgcc gaaaagaggg 60
 gcctccgagc cgccggcgcc ctctgccggc aacctccgga agcacactag gaggttccag 120
 ccgatctggt cgaggggctc cacggaggac tccatttacg ttacgcaa at tccctacccc 180
 agccggccgg agagagaaaag ccagaaacct cgcgaccagc catggggccac ctctccggaa 240
 aaacaccggg atattttttt tctcctgcag aaaaagcttt aggattggca gtttaaacia 300
 aacatgtcta tttgcatacc ttcgggtttgc atgcatttgt ttcgaagtga gcaaccctgg 360
 gtaacaaggc gaaagtatat gacaatttgc tcagaatctt aatgtcagaa aactggagac 420
 tggggcaggg ggggtgtcgac tcaaagctgt gtctcattta gtaaaactgag gccaggtaa 480
 aaagtcttga aacctcgcaa caccgggaga aattgtgttc cagcctccca cctcgcccca 540
 aaatgccaga gctccttttc taagccaggt gaagtcacag agcgtggaca gaaccacaaa 600
 ccgtccagag gaagggtcac tgggtgccac ctgggtttgca tctgtgcctt cgtcctgccc 660
 agttcctgag tgggaccgca ggcccggaa gtcaaggcaa acagtcctgc ttcagccact 720
 gggctccagt cccaccctt ttgggggcct gaagttagga agcatccggc agctgccttc 780
 tatttaagca actggcctcc tttagaggcca ctccctggcc atgccaggcg cgggcatctg 840
 gccagcatgc tgctctgcac ggctcgccctg gtccggcctgc agcttctcat ttcctgctgc 900
 tgggcctttg cctgccatag cacggagtct tctcctgact tcaccctccc cggagattac 960
 ctccctggcag gcctgttccc tctccattct ggctgtctgc aggtgaggca cagacccgag 1020
 gtgaccctgt gtgacaggtg agtgaggggc cagcagagcc acacttagtg ggacccttg 1080
 ctatagggcc cctctggctg ccatectcca aacaggacct tgcccttgcc tttgccccct 1140
 gaactgtccc caggccttgt tcatcaatcc acttgccacc taagtgtctg ctagaccttc 1200
 ctagacactt cggccagttt ccaattattt cacccttgct gttagaatgt nnnnnnnnnn 1260
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn aattccttaa actaaatttc 1320
 tcactttctc tctctctctg gaaaacactg actaatgtag caggtttctc tgctccagga 1380
 cttcaggacc ttttcgatgc taataagttt ctccatcagg gccagcttgt tctcctact 1440
 gagcttgaga gcccttgttg aagttgtggt ttgggggact ggaccgatga cctcaaagg 1500
 tccctttgct cccaagcctc agagtctagg aggcagagg gtctcagcag gcctttgtcc 1560
 ttctcagctg tctcttactg gctttctcca caggctctgt agcttcaatg agcatggcta 1620
 ccacctcttc caggctatgc ggcttggggg tgaggagata aacaactcca cggccttgct 1680
 gcccaacatc accctggggg accagctgta tgatgtgtgt tctgactctg ccaatgtgta 1740
 tgccacgctg agagtgtctt ccctgccagg gcaacaccac atagagctcc aaggagacct 1800
 tctccactat tcccctacgg tgctggcagt gattgggcct gacagacca accgtgctgc 1860
 caccacagcc gccctgctga gccctttcct ggtgcccctg gtaagctgga gcctcagacc 1920
 tttgcccctc tcccttcagg caagtctggg nnnnnnnnnn nnnnnnnnnn 1980
 nnnnnnnnnn nnnnnnnnnn gccaccatgc ccggctaatt tttttgtatt tttagtagag 2040
 acgggggttc accgtgttag ccaggctggt cgcaaactcc taacctctg atccaccac 2100
 ctgggcctcc caatgtgctg ggattacagg tgtgagccac tgcaccggc cataatgtat 2160
 taatataata aaataattat acaactcacc ataatgtaga atcagtgga gccctgagct 2220
 tgttttccca caactagatg gtcccatctg ggggtgatgg gagacagtga cagatcatca 2280
 gacattagat tctcataagt agcgtgcaac ccagatccct cgcagtgtga gttcacagta 2340
 ggggttcaagc tctacaaga atctgatgct gctgctgac tgacaggagg ggagcagctg 2400
 taaatacaga tgaagcttcg ctactcacc agctgtcac ctccctctgt gaggccggg 2460
 tccaaacagg ccactgacct aacttctgcc ctgacctaca catgcttctc tcttctcttg 2520

caaactgcct	ccagtgggaag	tccctgaag	tcccaaaaca	cacgggacta	tttcactcct	2580
atgcagggtt	tgtctccttt	gcttggaatg	catccctca	ccccttgtcc	ccaggcagat	2640
tcccacccct	ccccagaac	ctgccccagt	ggagccttcg	cagggtgatt	gtcagtttca	2700
caggctgagg	ggtgctctcc	tggctcccc	ggctccctgt	atccccacac	ccagcacagg	2760
gccaggcact	gggggggcct	tcagtggaga	ctgaaatggc	tgaacgggac	ctcccataga	2820
ttagctatgc	ggccagcagc	gagacgctca	gcgtgaagcg	gcagtatccc	tctttcctgc	2880
gcaccatccc	caatgacaag	taccaggtgg	agaccatggg	gctgctgctg	cagaagtctg	2940
ggtggacctg	gatctctctg	gttggcagca	gtgacgacta	tgggcagcta	ggggtgcagg	3000
cactggagaa	ccaggccact	ggtcagggga	tctgcattgc	tttcaaggac	atcatgccct	3060
tctctgcccc	ggtgggcgat	gagaggatgc	agtgcctcat	gcgccacctg	gcccaggccg	3120
ggggccaccgt	cgtggttggt	ttttccagcc	ggcagttggc	cagggtgttt	ttcaggtccg	3180
tgggtgctgac	caacctgact	ggcaagggtg	gggtcgccctc	agaagcctgg	gcctctcca	3240
ggcacatcac	tggggtgccc	gggatccagc	gcattgggat	ggtgctgggc	gtggccatcc	3300
agaagagggc	tgtccctggc	ctgaaggcgt	ttgaagaagc	ctatgcccg	gcagacaaga	3360
aggcccttag	gccttgccac	aagggtcctc	ggtgcagcag	caatcagctc	tgcagagaat	3420
gccaagcttt	catggcacac	acgatgccc	agctcaaagc	cttctccatg	agttctgcct	3480
acaacgcata	ccgggctgtg	tatgcggtgg	cccatggcct	ccaccagctc	ctgggctgtg	3540
cctctggagc	ttgttccagg	ggccgagctc	acccctggca	ggtaagagag	cccacccag	3600
cacctcctgt	caggggagaac	agccaatcct	gagatgagca	gagtgggcac	tctccggtca	3660
ctctaaatgc	caagggggat	aaatgccact	aacttgaggt	tttttgtttt	gttttgtttt	3720
gttttttgag	acagtctggc	tctgtcacc	aggctgcagt	gtagtgatgc	gatctcggct	3780
ctctgcaact	tccacctcct	gggttcaagt	gattctcttg	cctcggcctc	ctgagtagct	3840
gggattacag	gcccccacca	ccatgcctgg	ataatttttc	ttttcttttt	tttttttttg	3900
agatagagtc	tcgctctgtt	gcccaggctg	gaatgcagtg	gtgcgatctt	ggctcattgt	3960
gagctccgcc	tcccagggtt	actccattcc	cctgcctcag	cctcccaagt	aggtgggact	4020
acgggcgcgc	gccaccacgc	ccagctaatt	ttttttgtat	tttgagtaga	gacgggggtt	4080
caccatgtta	gccaggatgg	tctcaatctc	ctgacctgt	catccgcccc	cctcgtcctc	4140
ccaaagtgtc	gggattacag	gcgtgagcca	ccgcaccgg	cctaattttt	gtatttttag	4200
tagagatggg	gtttcaccat	gttgcccagg	ctggtctcga	actcctggca	tcaagtgatc	4260
ctcctgcttc	ggcctcccaa	agtgtcggga	ttacaggcat	tagctctctt	ctcttagaca	4320
gatctttctc	tctgatcctt	gccttctctc	acccactgtg	tcttgggaagt	gtcaagtgat	4380
aagatccagg	gctaaaactg	tctgtaaagg	agtgtttgtt	agaggcctcc	tctcaggagg	4440
ttggtgggga	agattgaggg	gcttcctaag	aagggaaggga	cgagaccttc	ctgatgggct	4500
gaaaccacca	ggacggaaac	ccaggaaggc	cccaggccct	tgccttctggg	accatgtggg	4560
tctgtgctgt	ctgtgggtgg	ttcatgatac	gcgtttcttt	cagcttttgg	agcagatcca	4620
caagggtgcat	ttccttctac	acaaggacac	tgtggcgttt	aatgacaaca	gagatcccc	4680
cagtagctat	aacataattg	cctgggactg	gaatggaccc	aagtggacct	tcacggctct	4740
cggttcctcc	acatggtctc	cagttcagct	aaacataaat	gagaccaaaa	tccagtggca	4800
cggaaaggac	aaccaggtaa	tggggatgtg	gctactcacc	atgtaactgg	cttatgggca	4860
acctagagcc	tgggggtgat	gctgacacag	tgtacaggga	gcaggagggg	ggccccaggg	4920
gtccagctgc	caccactcta	cccatcctgg	ccagggaagc	agggaagaca	ctccgtaggc	4980
gagtgtgcag	atgccctggg	gcggaagttc	acacgaccag	gggccctgcc	ctgggagtga	5040
gccctgaggg	cagatgcaca	gagattctgt	tttctgttcc	acatgtgagc	tgtcctttga	5100
cttgggcccc	tacgtgtggc	ccctctggct	tcttacaggt	gcctaagtct	gtgtgttcca	5160
gcgactgtct	tgaagggcac	cagcgagtgg	ttacgggttt	ccatcactgc	tgtcttgagt	5220
gtgtgccctg	tggggctggg	accttctctc	acaagagtgg	tgagtgggca	atggagcagg	5280
cgagctaccc	agcactccc	ggggctgcac	ggtggaggga	gggcctccct	tgggccccat	5340
gtgccctgcc	ccagaaccaa	ggcccagtca	ctgggctgcc	agttagcttc	aggttggagg	5400
acacctgcta	ccagacagaa	ttctgatcaa	gagaatcagc	cactgggtgc	ggtggctcat	5460
gcctgtaatc	ccagcacttt	gggaggctga	ggcgggtgga	tcacttgagg	tcgggagttc	5520
gagaccagcc	tggccaacat	ggtgaaaccc	catctctacc	aaaaatataa	aaaattagct	5580
gggtgtgggt	gcgcgtgcct	gtaatcccag	ctactcggga	ggctgaggga	ggagaatcac	5640
ttgaaccagg	gaggcggagg	ttgcagttag	ccaagatgca	ttccagcctg	gaccacaaag	5700
cgagaattcg	tcccccaaaa	aaaagaaagg	aggccgggcg	cgggtggctca	cacctgtaat	5760
cccagcactt	tgggaggccg	aggtgggtgg	atcacctgag	gtcaggaggt	cgagaccagc	5820
ctgaccaaca	tggtgaaacc	ccatctctac	taaaaataca	aaaaaagtta	gccgggcgtt	5880
gtggcgtgtg	cctgtaattc	cagctactcg	ggaggctgag	gcaggagaat	tgttgtaacc	5940
cgggaggcgg	aggttgagct	gagccaagat	tgcaccattg	cactccagcc	tgggcgacaa	6000

gagaaaaact	ctgtctcaaa	aaaaaagaaa	gaaagaaaga	attagccaac	tgaaagcctt	6060
agactgaggt	gtgtcctctg	ttagagagct	gtcatcacaa	ctcctacaaa	agcagtcgta	6120
tcctgaattc	aacctctttc	tctaaatgaa	tatagctatt	gttccctttg	tgccctcttg	6180
tcctactgtc	ccttctgttg	cccatgccaa	agacagctag	ctccttgaac	agcttggcct	6240
gaatacagat	actagcgtgt	ctgcagcaga	gaaaaaaaca	gcattcccca	tccagaaatg	6300
caaggtcaag	aacagagagc	aaattaggta	gctaaggact	caggtcctta	gttgggtgtcc	6360
agggggccaca	ttctttcctt	tcaccatctc	tgtagggaca	ggaatacttc	ccttctgtcc	6420
tcagaggggtc	aggactcaga	gaaaccacag	agcagcagct	caggaaagtg	gttcatggaa	6480
atgctggcaa	gagagagggg	ttacaatgcc	ctcccttggg	agcaggctgc	tcccatcaga	6540
tcgtaacctc	tctgggtatgt	gggcagagct	accaggttaa	ggtcctccct	agggtttgca	6600
aaacctctcat	gggatcatga	gccatacaga	accgacctgt	gtgtctccag	agtctgtaat	6660
taacacagggc	attttgagga	aatgcgtggc	ctcaggcccc	actcccggct	accccatcc	6720
cactatgcct	agtatagtct	agctgccctg	gtacaattct	cccagtatct	tgcaggcccc	6780
tatttctctat	tcctactctg	ctcatctggc	tctcaggaac	cttcttggcc	ttccctttca	6840
gacctctaca	gatgccagcc	ttgtgggaaa	gaagagtggg	cacctgaggg	aagccagacc	6900
tgcttcccgc	gcactgtggt	gtttttggct	ttgcgtgagc	acacctcttg	ggtgctgctg	6960
gcagctaaca	cgctgctgct	gctgctgctg	cttgggactg	ctggcctgtt	tgcctggcac	7020
ctagacaccc	ctgtggtgag	gtcagcaggg	ggcgcctgt	gctttcttat	gctgggctcc	7080
ctggcagcag	gtagtggcag	cctctatggc	ttctttgggg	aaccacaaag	gcctgcgtgc	7140
ttgctacgcc	aggccctctt	tgcccttggg	ttcaccatct	tcctgtcctg	cctgacagtt	7200
cgctcatctc	aactaatcat	catcttcaag	ttttccacca	aggtacctac	attctaccac	7260
gacctgggtcc	aaaaccacgg	tgctggcctg	tttgtgatga	tcagctcagc	ggcccagctg	7320
cttatctgtc	taacttggct	ggtggtgtgg	acccactgc	ctgctagggg	ataccagcgc	7380
ttcccccatc	tggtgatgct	tgagtgcaca	gagaccaact	ccctgggctt	catactggcc	7440
ttcctctaca	atggcctcct	ctccatcagt	gcctttgcct	gcagctacct	gggtaaggac	7500
ttgccagaga	actacaacga	ggccaaatgt	gtcaccttca	gcctgctctt	caacttcgtg	7560
tcttggtatcg	ccttcttcac	cacggccagc	gtctacgacg	gcaagtacct	gcctgcggcc	7620
aacatgatgg	ctgggctgag	cagcctgagc	agcggcttcg	gtgggtatgt	tctgcctaag	7680
tgctacgtga	tcctctgccc	cccagacctc	aacagcacag	agcacttcca	ggcctccatt	7740
caggactaca	cgaggcgctg	cggctccacc	tgaccagtgg	gtcagcaggc	acggctggca	7800
gccttctctg	ccctgagggg	cgaaggctga	gcaggccggg	ggtgtccggg	aggtctttgg	7860
gcatcgcggt	ctgggggttg	gacgtgtaag	cgcctgggag	agcctagacc	aggctccggg	7920
ctgccaaataa	agaagtgaag	tgcgatatctg	gtctcctgtc	gtgggagagt	gtgaggtgta	7980
acggattcaa	gtctgaaccc	agagcctgga	aaaggctgac	cgcccagatt	gacgttgcta	8040
ggcaactccg	gaggcggggc	cagcgccaaa	agaacagggc	gaggcgctcg	ccccgcatcc	8100
cattggccgt	tctctgcggg	gccccgcctt	cgggggcccgg	agctagaagc	tctacgcttc	8160
cgaggcgcac	ctcctggcct	gcacgctttg	acgt			8194

<210> 16

<211> 2526

<212> DNA

<213> Homo sapiens

<400> 16

atgctgctct	gcacggctcg	cctggctcggc	ctgcagcttc	tcatttctctg	ctgctggggcc	60
tttgccctgcc	atagcacgga	gtcttctcct	gacttcaccc	ttcccggaga	ttacctcttg	120
gcaggcctgt	tcctctcca	ttctggctgt	ctgcagggtga	ggcacagacc	cgaggtgacc	180
ctgtgtgaca	ggtcttgtag	cttcaatgag	catggctacc	acctcttcca	ggctatgcgg	240
cttgggggttg	aggagataaa	caactccacg	gccctgctgc	ccaacatcac	cctgggggtac	300
cagctgtatg	atgtgtgttc	tgactctgcc	aatgtgtatg	ccacgctgag	agtgtctctcc	360
ctgccagggc	aacaccacat	agagctccaa	ggagaccttc	tccactattc	ccctacgggtg	420
ctggcagtgga	ttgggcctga	cagcaccaac	cgtgctgcca	ccacagccgc	cctgctgagc	480
cctttctctg	tgcccatgat	tagctatgcg	gccagcagcg	agacgctcag	cgtgaagcgg	540
cagtatccct	ctttctctgcg	caccatcccc	aatgacaagt	accaggtgga	gaccatgggtg	600
ctgctgctgc	agaagtctcg	gtggacctgg	atctctctgg	ttggcagcag	tgacgactat	660
gggcagctag	gggtgcaggc	actggagaac	caggccactg	gtcaggggat	ctgcattgct	720
ttcaaggaca	tcatgccttt	ctctgcccag	gtggggcgatg	agaggatgca	gtgcctcatg	780

cgccacctgg cccaggccgg ggccaccgtc gtgggtgttt tttccagccg gcagttggcc 840
 aggggtgttt tcgagtcctg ggtgctgacc aacctgactg gcaaggtgtg ggtcgccctca 900
 gaagcctggg cctctccag gcacatcact ggggtgcccg ggatccagcg cattgggatg 960
 gtgctggggc tggccatcca gaagagggt gtccctggcc tgaaggcgtt tgaagaagcc 1020
 tatgcccggg cagacaagaa ggcccctagg ccttgccaca agggctcctg gtgcagcagc 1080
 aatcagctct gcagagaatg ccaagctttc atggcacaca cgatgcccga gctcaaagcc 1140
 ttctccatga gttctgccta caacgcatac cgggctgtgt atgcggtggc ccatggcctc 1200
 caccagctcc tgggctgtgc ctctggagct tgttccaggg gccgagtcta cccctggcag 1260
 cttttggagc agatccacaa ggtgcatttc cttctacaca aggacactgt ggcgtttaat 1320
 gacaacagag atccctcag tagctataac ataattgcct gggactggaa tggacccaag 1380
 tggaccttca cggctcctcg ttctccaca tggctccag ttcagctaaa cataaatgag 1440
 accaaaatcc agtggcacgg aaaggacaac cagggtgccta agtctgtgtg ttccagcgac 1500
 tgtcttgaag ggcaccagcg agtggttacg ggtttccatc actgctgctt tgagtgtgtg 1560
 ccctgtgggg ctgggacctt cctcaacaag agtgacctct acagatgcca gccttgtggg 1620
 aaagaagagt gggcacctga gggaagccag acctgcttcc cgcgcactgt ggtgtttttg 1680
 gctttgcgtg agcacacctc ttgggtgctg ctggcagcta acacgctgct gctgctgctg 1740
 ctgcttggga ctgctggcct gtttgctgg cacctagaca cccctgtggt gaggtcagca 1800
 gggggccgcc tgtgctttct tatgctgggc tccctggcag caggtagtgg cagcctctat 1860
 ggcttctttg gggaaacccac aaggcctgcg tgcctgctac gccaggccct ctttgccctt 1920
 ggtttcaoca tcttctgtc ctgcctgaca gtctgctcat tccaactaat catcatcttc 1980
 aagttttcca ccaaggtacc tacattctac cagcctggg tccaaaacca cgggtgctggc 2040
 ctgtttgtga tgatcagctc agcggcccg ctgcttatct gtctaacttg gctggtgggtg 2100
 tggacccccc tgcctgctag ggaataccag cgcttcccc atctggtgat gcttgagtgc 2160
 acagagacca actccctggg cttcatactg gccttccctt acaatggcct cctctccatc 2220
 agtgcctttg cctgcagcta cctgggtaag gacttgccag agaactacaa cgaggccaaa 2280
 tgtgtcacct tcagcctgct cttcaacttc gtgtcctgga tcgccttctt caccacggcc 2340
 agcgtctacg acggcaagta cctgcctgcg gccaacatga tggctgggct gaggcagctg 2400
 agcagcggct tcggtgggta ttttctgcct aagtgtacg tgatcctctg ccgcccagac 2460
 ctcaacagca cagagcactt ccaggcctcc attcaggact acacgaggcg ctgcggctcc 2520
 acctga 2526

<210> 17

<211> 841

<212> PRT

<213> Homo sapiens

<400> 17

Met Leu Leu Cys Thr Ala Arg Leu Val Gly Leu Gln Leu Leu Ile Ser
 1 5 10 15

Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
 20 25 30

Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
 35 40 45

Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
 50 55 60

Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
 65 70 75 80

Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
 85 90 95

Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
 100 105 110

Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu
 115 120 125
 Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile
 130 135 140
 Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser
 145 150 155 160
 Pro Phe Leu Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu
 165 170 175
 Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp
 180 185 190
 Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp
 195 200 205
 Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly
 210 215 220
 Val Gln Ala Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala
 225 230 235 240
 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
 245 250 255
 Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val
 260 265 270
 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
 275 280 285
 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala
 290 295 300
 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
 305 310 315 320
 Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
 325 330 335
 Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys
 340 345 350
 His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
 355 360 365
 Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
 370 375 380
 Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
 385 390 395 400
 His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val
 405 410 415

Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
 420 425 430
 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
 435 440 445
 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
 450 455 460
 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
 465 470 475 480
 Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
 485 490 495
 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
 500 505 510
 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
 515 520 525
 Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp
 530 535 540
 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
 545 550 555 560
 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
 565 570 575
 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
 580 585 590
 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
 595 600 605
 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
 610 615 620
 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
 625 630 635 640
 Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
 645 650 655
 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
 660 665 670
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
 675 680 685
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
 690 695 700
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
 705 710 715 720

<220>
 <221> MOD_RES
 <222> (8)
 <223> Val, Glu, Arg, Lys or Thr

<220>
 <221> MOD_RES
 <222> (11)
 <223> Ala or Glu

<220>
 <221> MOD_RES
 <222> (12)
 <223> Trp or Leu

<220>
 <221> MOD_RES
 <222> (13)
 <223> Arg, His or Gly

<400> 18
 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
 1 5 10

<210> 19
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)
 <223> Leu or Gln

<220>
 <221> MOD_RES
 <222> (3)
 <223> Glu, Gly or Thr

<220>
 <221> MOD_RES
 <222> (4)
 <223> Asn, Arg or Cys

<220>
 <221> MOD_RES
 <222> (7)
 <223> Arg or Glu

<220>
 <221> MOD_RES
 <222> (9)

<223> Arg or Lys

<220>

<221> MOD_RES

<222> (10)

<223> Cys, Gly or Phe

<220>

<221> MOD_RES

<222> (11)

<223> Val, Leu or Ile

<220>

<221> MOD_RES

<222> (13)

<223> Phe or Leu

<220>

<221> MOD_RES

<222> (14)

<223> Ala or Ser

<220>

<221> MOD_RES

<222> (15)

<223> Met or Leu

<400> 19

Xaa	Pro	Xaa	Xaa	Tyr	Asn	Xaa	Ala	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Xaa
1				5					10					15

<210> 20

<211> 3563

<212> DNA

<213> Homo sapiens

<400> 20

agcctggcag	tggcctcagg	cagagtctga	cgcgcacaaa	ctttcaggcc	caggaagcga	60
ggacaccact	ggggccccag	ggtgtggcaa	gtgaggatgg	caagggtttt	gctaaacaaa	120
tcctctgccc	gctccccgcc	ccgggctcac	tccatgtgag	gccccagtcg	gggcagccac	180
ctgccgtgcc	tgttggaagt	tgcctctgcc	atgctgggcc	ctgctgtcct	gggcctcagc	240
ctctgggctc	tcctgcaccc	tgggacgggg	gccccattgt	gcctgtcaca	gcaacttagg	300
atgaaggggg	actacgtgct	gggggggctg	ttccccctgg	gcgaggccga	ggaggctggc	360
ctccgcagcc	ggacacggcc	cagcagccct	gtgtgcacca	ggtacagagg	tgggacggcc	420
tgggtcgggg	tcagggtgac	caggtctggg	gtgctcctga	gctggggccg	aggtggccat	480
ctgcggttct	gtgtggcccc	aggttctcct	caaacggcct	gctctgggca	ctggccatga	540
aaatggccgt	ggaggagatc	aacaacaagt	cggatctgct	gcccgggctg	cgcctgggct	600
acgacctctt	tgatacgtgc	tcggagcctg	tggtggccat	gaagcccagc	ctcatgttcc	660
tggccaaggc	aggcagccgc	gacatcgccg	cctactgcaa	ctacacgcag	taccagcccc	720
gtgtgctggc	tgtcatcggg	ccccactcgt	cagagctcgc	catgggtcacc	ggcaagttct	780
tcagcttctt	cctcatgccc	cagtggggcg	ccccccacca	tcacccaccc	ccaaccaacc	840
cctgccccgt	gggagccctt	tgtgtcagga	gaatgctaca	tgcacccccc	ccagcctgc	900
cctgggagcc	ctgtgtcaga	agatgctcct	ggccttgtag	gtcagctacg	gtgctagcat	960
ggagctgctg	agcgcccggg	agacctcccc	ctccttcttc	cgcaccgtgc	ccagcgaccg	1020
tgtgcagctg	acggccgccc	cggagctgct	gcaggagtgc	ggctggaact	gggtggccgc	1080
cctgggcagc	gacgacgagt	acggccggca	gggcctgagc	atcttctcgg	ccctggccgc	1140
ggcacgcggc	atctgcatcg	cgcacgaggg	cctggtgccg	ctgccccgtg	ccgatgaact	1200

```

gcggctgggg aaggtgcagg acgtcctgca ccaggtgaac cagagcagcg tgcaggtggt 1260
gctgctgttc gcctccgtgc acgccgccca cgccctcttc aactacagca tcagcagcag 1320
gctctcgccc aaggtgtggg tggccagcga ggcttggtg acctctgacc tggatcatggg 1380
gctgcccggc atggcccaga tgggcacggg gcttggcttc ctccagaggg gtgcccagct 1440
gcacgagttc cccagtagc tgaagacgca cctggccctg gccaccgacc cggccttctg 1500
ctctgccttg ggcgagaggg agcaggtct ggaggaggac gtggtggggc agcgtgccc 1560
gcagtgtgac tgcatacagc tgcagaacgt gagcgaggg ctaaatacacc accagacgtt 1620
ctctgtctac gcagctgtgt atagcgtggc ccaggccctg cacaacactc ttcagtgc aa 1680
cgctcaggc tgcctcgccg aggaccccg gaagccctgg caggtgagcc cgggagatgg 1740
gggtgtgctg tcctctgcat gtgccaggc caccaggcac ggccaccag cctgagctgg 1800
aggtggctgg cggctcagcc ccgtccccc cccgcagctc ctggagaaca tgtacaacct 1860
gaccttccac gtgggcccggc tgcctgtgct gttcgacagc agcggaaacg tggacatgga 1920
gtacgacctg aagctgtggg tgtggcaggg ctcatgtccc aggtctccag acgtggggcag 1980
gttcaacggc agcctcagga cagagcgct gaagatccgc tggcacacgt ctgacaacca 2040
ggtgaggtga ggggtgggtgt gccaggcgtg cccgtggtag ccccccgcgc agggcgagc 2100
ctgggggtgg gggccgttcc agtctcccg tggcatgccc agccgagcag agccagacct 2160
caggcctgtg cgcagaagcc cgtgtcccgg tgctcgccg agtgccagga gggccaggtg 2220
cgccgggtca aggggttcca ctctgtgctg tactactgtg tggactgca ggcggggcag 2280
taccggcaaa acccaggtga gccgccttcc cggcaggcgg ggggtgggaac gcagcagggg 2340
agggctcctg caagtccctga ctctgagacc agagcccaca gggtagaaga cgaacaccca 2400
gcgcccttct cctctctcac agacgacatc gcctgcacct tttgtggcca ggatgagtg 2460
tccccggagc gaagcacacg ctgcttccgc cgcaggtctc ggttcctggc atggggcgag 2520
ccggctgtgc tgcctgtgct cctgtgtgct agcctggcgc tgggccttgt gctggctgt 2580
ttggggctgt tcgttcacca tcgggacagc ccactggttc aggcctcggg gggggccctg 2640
gcctgtcttg gcctggtgtg cctgggcctg gtctgectca gcgtcctcct gttccctggc 2700
cagcccagcc ctgcccgatg cctggcccag cagcccttgt cccacctccc gctcacgggc 2760
tgctgagca cactcttct gcaggcggcc gagatcttcg tggagtca ga actgcctctg 2820
agctgggcag accggctgag tggctgctg cgggggcccct gggcctggct ggtggtgctg 2880
ctggccatgc tgggtggagg cgcactgtgc accctgtacc tgggtggcct cccgcggag 2940
gtggtgacgg actggcacat gctgccacg gaggcgctgg tgactgccc caccgctcc 3000
tgggtcagct tcggcctagc gcacgccacc aatgccacgc tggcctttct ctgcttctg 3060
ggcactttcc tgggtcggag ccagccgggc tgctacaacc gtgcccgtg cctcaccttt 3120
gccatgctgg cctacttcat cacctgggtc tcctttgtgc cctcctggc caatgtgcag 3180
gtggtcctca gggccgcccgt gcagatgggc gccctcctgc tctgtgtcct gggcatcctg 3240
gctgcccctc acctgccag gtgttacct ctcactgcgg agccagggct caacaccccc 3300
gagttcttcc tgggaggggg cctggggat ccccaaggcc agaatagcgg gaacacagga 3360
aatcagggga aacatgagtg acccaacct gtgatctcag ccccggtgaa cccagactta 3420
gctgcgatcc cccccaagcc agcaatgacc cgtgtctcgc tacagagacc ctcccgtct 3480
aggttctgac cccaggttgt ctctgaccc tgacccaca gtgagcccta ggcctggagc 3540
acgtggacac ccctgtgacc atc
3563

```

<210> 21

<211> 839

<212> PRT

<213> Homo sapiens

<400> 21

```

Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
  1                      5                      10                      15

Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
                20                      25                      30

Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
    35                      40                      45

```

Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
 50 55 60
 Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
 65 70 75 80
 Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr
 85 90 95
 Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu
 100 105 110
 Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr
 115 120 125
 Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser
 130 135 140
 Glu Ser Val Met Thr Val Ala Asn Phe Leu Ser Leu Phe Leu Leu Pro
 145 150 155 160
 Gln Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg
 165 170 175
 Phe Pro Ala Leu Leu Arg Thr Thr Pro Ser Ala Asp His His Val Glu
 180 185 190
 Ala Met Val Gln Leu Met Leu His Phe Arg Trp Asn Trp Ile Ile Val
 195 200 205
 Leu Val Ser Ser Asp Thr Tyr Gly Arg Asp Asn Gly Gln Leu Leu Gly
 210 215 220
 Glu Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu
 225 230 235 240
 Pro Thr Leu Gln Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg
 245 250 255
 Leu Val Thr Ile Val Asp Lys Leu Gln Gln Ser Thr Ala Arg Val Val
 260 265 270
 Val Val Phe Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val
 275 280 285
 Leu Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp
 290 295 300
 Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu Gly His Leu Gly
 305 310 315 320
 Thr Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser
 325 330 335
 Glu Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg
 340 345 350

Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn
 355 360 365
 Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val
 370 375 380
 Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His
 385 390 395 400
 Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu
 420 425 430
 Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu
 435 440 445
 Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser
 450 455 460
 Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp
 465 470 475 480
 Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser
 485 490 495
 Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val
 500 505 510
 Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His
 515 520 525
 Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser
 530 535 540
 Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu
 545 550 555 560
 Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Ala Leu Gly
 565 570 575
 Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln
 580 585 590
 Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu
 595 600 605
 Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro
 610 615 620
 Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys
 625 630 635 640
 Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val
 645 650 655

Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
 660 665 670
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
 675 680 685
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro
 690 695 700
 Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys
 705 710 715 720
 Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu
 725 730 735
 Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu
 740 745 750
 Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe
 755 760 765
 Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser
 770 775 780
 Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu
 785 790 795 800
 Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu
 805 810 815
 Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln
 820 825 830
 Gly Tyr Thr Met Arg Arg Asp
 835

<210> 22
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 PDZIP peptide sequence

<400> 22
 Ser Val Ser Thr Val Val
 1 5

<210> 23
 <211> 2520
 <212> DNA
 <213> Homo sapiens

<400> 23
 atggggcccca gggcaaagac catctgctcc ctgttcttcc tcctatgggt cctggctgag 60

```

ccggctgaga actcggactt ctacctgect ggggattacc tcctgggtgg cctcttctcc 120
ctccatgccca acatgaaggg cattgttcac cttaacttcc tgcaggtgcc catgtgcaag 180
gagtatgaag tgaaggtgat aggctacaac ctcatgcagg ccatgcgctt cgcggtggag 240
gagatcaaca atgacagcag cctgctgect ggtgtgctgc tgggctatga gatcgtggat 300
gtgtgctaca tctccaacaa tgtccagccg gtgctctact tcctggcaca cgaggacaac 360
ctccttccca tccaagagga ctacagtaac tacatttccc gtgtggtggc tgtcattggc 420
cctgacaact ccgagttctgt catgactgtg gccaaacttcc tctccctatt tctccttcca 480
cagatcacct acagcgccat cagcgatgag ctgcgagaca aggtgcgctt cccggctttg 540
ctgctgacca caccagcgc cgaccaccac gtcgaggcca tgggtgcagct gatgctgcac 600
ttccgctgga actggatcat tgtgctgggtg agcagcgaca cctatggccg cgacaatggc 660
cagctgcttg gcgagcgctg ggcccggcgc gacatctgca tcgccttcca ggagacgctg 720
cccacactgc agcccaacca gaacatgacg tcagaggagc gccagcgctt ggtgaccatt 780
gtggacaagc tgcagcagag cacagcgctg gtcgtgggtg tgttctcgcc cgacctgacc 840
ctgtaccact tcttcaatga ggtgctgctg cagaacttca cgggcgcctg gtggatcgcc 900
tccgagtcct gggccatcga cccggtcctg cacaacctca cggagctggg ccacttgggc 960
accttctctg gcatcaccat ccagagcgtg cccatcccgg gcttcagtga gttccgagag 1020
tggggcccac aggtcgggccc gccacccctc agcaggacca gccagagcta tacctgcaac 1080
caggagtgcg acaactgcct gaacgccacc ttgtccttca acaccattct caggctctct 1140
ggggagcgtg tgcgtctacag cgtgtactct ggggtctatg ctgtggccca tgccctgcac 1200
agcctcctcg gctgtgacaa aagcacctgc accaagaggg tggcttacc cgtggcagctg 1260
cttgaggaga tctggaaggt caacttcaact ctccctggacc accaaatctt cttcgacctg 1320
caaggggacg tggctctgca cttggagatt gtccagtggc aatgggaccg gagccagaat 1380
cccttccaga gcgtcgccctc ctactacccc ctgcagcgac agctgaagaa catccaagac 1440
atctcctggc acaccgtcaa caacacgatc cctatgtcca tgtgttccaa gaggtgccag 1500
tcagggcaaa agaagaagcc tgtgggcatc cacgtctgct gcttcgagtg catcgactgc 1560
cttcccggca ccttccctcaa ccacactgaa gatgaatatg aatgccaggc ctgcccgaat 1620
aacgagtggc cctaccagag tgagacctcc tgcctcaagc ggcagctggg cttcctggaa 1680
tggcatgagg caccaccat cgctgtggcc ctgctggccg ccctgggctt cctcagcacc 1740
ctggccatcc tgggtgatatt ctggaggcac ttccagacac ccatagttcg ctcggtggg 1800
ggcccatgt gcttccctgat gctgacactg ctgctgggtg catacatggt ggtcccgtg 1860
tacgtggggc cgcccaaggt ctccacctgc ctctgccgcc aggccctctt tcccctctgc 1920
ttcacaattt gcatctcctg tatcgccgtg cgttctttcc agatcgtctg cgccttcaag 1980
atggccagcc gcttcccacg cgccctacagc tactgggtcc gctaccaggg gccctacgtc 2040
tctatggcat ttatcacggt actcaaatg gtcattgtgg taattggcat gctggccacg 2100
ggcctcagtc ccaccacccg tactgacccc gatgaccca agatcacaat tgtctcctgt 2160
aaccccaact accgcaacag cctgctgttc aacaccagcc tggacctgct gctctcagtg 2220
gtgggtttca gcttcgccta catgggcaaa gagctgcca ccaactacaa cgaggccaag 2280
ttcatcacc tcagcatgac cttctatttc acctatccg tctccctctg caccttcatg 2340
tctgcctaca gcgggggtgct ggtcaccatc gtggacctct tggtcactgt gctcaacctc 2400
ctggccatca gcctgggcta cttcgccccc aagtgtctaca tgatcctctt ctaccggag 2460
cgcaacacgc ccgcctactt caacagcatg atccagggt acaccatgag gagggactag 2520

```

<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Six-His tag

<400> 24

His His His His His His

1

5